

Genforce version 4.5  
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04 nucleotide nucleotide search, using sw model

Run on: September 26, 2002, 09:00:46 : Search time 93.9 Seconds

(without alignments)  
3913.394 Million cell updates/sec

Hit: US-10-006-430-3  
Footest score: 1496  
Sequence: 1 ccat-gtgcgtgaaagcgc.....tgcctaaaaaanaaaaaa 1496

Scoring table:  
IDENTITY\_NUC  
Gap: 10.0, Gapext 1.0

Search: 48434 seqs, 122816752 residues

at number of hits satisfying chosen parameters: 478554

Minimum DB seq length: 16  
Maximum DB seq length: 50

Post processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: Issued parent's NA:  
2: /seq2\_6/prodata/2/ina/5A\_COMB.seq\*\*  
3: /seq2\_6/prodata/2/ina/5B\_COMB.seq\*\*  
4: /seq2\_6/prodata/2/ina/6A\_COMB.seq\*\*  
5: /seq2\_6/prodata/2/ina/6B\_COMB.seq\*\*  
6: /seq2\_6/prodata/2/ina/backfilst1.seq\*\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	24.4	1.6	50	1	US-08-171-389-331	Sequence 331, App
2	24.4	1.6	50	1	US-08-123-936-331	Sequence 331, App
3	24.4	1.6	50	2	US-08-475-228A-331	Sequence 331, App
4	24.4	1.6	50	5	US-08-482-080A-331	Sequence 331, App
5	24.4	1.6	50	5	PCT US94-12388-331	Sequence 331, App
6	24.4	1.6	50	1	US-08-171-389-374	Sequence 374, App
7	24.4	1.6	50	1	US-08-123-936-374	Sequence 374, App
8	24.4	1.6	50	2	US-08-475-228A-374	Sequence 374, App
9	24.4	1.6	50	5	US-08-482-080A-374	Sequence 374, App
10	24.4	1.6	50	5	PCT US94-12388-374	Sequence 374, App
11	24.4	1.6	40	4	US-09-677-045-10	Sequence 10, Appl
12	22.8	1.5	49	4	US-09-007-005-14	Sequence 14, Appl
13	22.8	1.5	49	4	US-09-244-796-14	Sequence 14, Appl
14	22.8	1.5	50	1	US-09-128-354-17	Sequence 17, Appl
15	22.4	1.5	49	1	US-08-171-389-267	Sequence 267, App
16	22.4	1.5	49	1	US-08-123-936-267	Sequence 267, App
17	22.4	1.5	49	2	US-08-475-228A-267	Sequence 267, App
18	22.4	1.5	49	4	US-08-482-080A-267	Sequence 267, App
19	22.4	1.5	49	5	PCT US94-12388-267	Sequence 267, App
20	22.2	1.5	43	3	US-08-726-807H-23	Sequence 23, Appl
21	22.2	1.5	43	3	US-09-258-467-23	Sequence 23, Appl
22	22.2	1.5	43	4	US-09-546-550-23	Sequence 23, Appl
23	22.2	1.5	43	4	US-09-441-414-23	Sequence 23, Appl
24	22.2	1.5	43	4	US-09-245-670-23	Sequence 23, Appl
25	22	1.5	43	4	US-09-007-005-16	Sequence 16, Appl
26	22	1.5	43	4	US-09-244-796-16	Sequence 16, Appl
27	21.8	1.5	50	4	US-09-165-264-4	Sequence 4, Appl

## ALIGNMENTS

28	21.4	1.4	39	4	US-09-306-290-40	Sequence 40, Appl
29	21.2	1.4	46	4	US-09-007-005-15	Sequence 15, Appl
30	21.2	1.4	46	4	US-09-244-796-15	Sequence 15, Appl
31	21.2	1.4	47	4	US-08-646-538-9	Sequence 9, Appl
32	21.2	1.4	47	4	US-09-503-222-9	Sequence 9, Appl
33	20.8	1.4	40	4	US-09-306-290-30	Sequence 30, Appl
34	20.6	1.4	35	1	US-08-435-350-118	Sequence 118, Appl
35	20.6	1.4	43	4	US-09-007-005-16	Sequence 16, Appl
36	20.6	1.4	46	4	US-09-244-796-16	Sequence 16, Appl
37	20.6	1.4	46	4	US-09-007-005-15	Sequence 15, Appl
38	20.6	1.4	48	2	US-08-618-911-10	Sequence 10, Appl
39	20.6	1.4	49	4	US-09-007-005-14	Sequence 14, Appl
40	20.6	1.4	49	4	US-09-244-796-14	Sequence 14, Appl
41	20.4	1.4	40	4	US-09-306-290-16	Sequence 16, Appl
42	20.4	1.4	50	1	US-08-171-389-481	Sequence 481, App
43	20.4	1.4	50	1	US-08-123-936-481	Sequence 481, App
44	20.4	1.4	50	2	US-08-475-228A-481	Sequence 481, App
45	20.4	1.4	50	2	US-08-475-228A-481	Sequence 481, App

RESULT 1  
US-08-171-389-331/C  
: Sequence 331, Application US/08171389  
: Patent No. 5578444  
: GENERAL INFORMATION:  
: APPLICANT: Edwards, Cynthia A.  
: APPLICANT: Cantor, Charles R.  
: APPLICANT: Andrews, Beth M.  
: APPLICANT: Turin, Lisa M.  
: APPLICANT: Fry, Kirk E.  
: TITLE OF INVENTION: Sequence-Directed DNA Binding  
: TITLE OF INVENTION: Molecules, Compositions and Methods  
: NUMBER OF SEQUENCES: 641  
: CORRESPONDENCE ADDRESS:  
: ADDRESS: Genclabs Technologies, Inc.  
: STREET: 505 Penobscot Drive  
: CITY: Redwood City  
: STATE: CA  
: COUNTRY: USA  
: ZIP: 94063  
: COMPUTER READABLE FORM: disk  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/171,389  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/123,936  
: FILING DATE: 17-Sep-1993  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/996,783  
: FILING DATE: 23-Dec-1992  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/723,618  
: FILING DATE: 27-Jun-1991  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/081,070  
: FILING DATE: 22-Jun-1993  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Fadian, Gary R.  
: REGISTRATION NUMBER: 33,875  
: REFERENCE/DOCKET NUMBER: 4600-0175/01914  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (415) 324-0980  
: TELEFAX: (415) 324-0960  
: INFORMATION FOR SEQ ID NO: 331:  
: SOURCE CHARACTERISTICS:







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1      COUNTRY:  USA
2      ZIP:      94063
3      COMPUTER READABLE FORM:
4      MEDIUM TYPE:  Floppy disk
5      COMPUTER:  IBM PC compatible
6      OPERATING SYSTEM:  PC-DOS/MS-DOS
7      SOFTWARE:  Patentin Release #1.0, Version #1.25
8      CURRENT APPLICATION NUMBER:  US/08/482,080A
9      APPLICATION NUMBER:  US/08/482,080A
10     FILING DATE:  07-JUN-1995
11     PRIOR APPLICATION DATA:
12     APPLICATION NUMBER:  US 08/171,389
13     FILING DATE:  20-DEC-1993
14     PRIOR APPLICATION DATA:
15     APPLICATION NUMBER:  US 08/123,936
16     FILING DATE:  17-SEP-1993
17     PRIOR APPLICATION DATA:
18     APPLICATION NUMBER:  US 07/996,783
19     FILING DATE:  23-DEC-1992
20     PRIOR APPLICATION DATA:
21     APPLICATION NUMBER:  US 07/723,618
22     FILING DATE:  27-JUN-1991
23     PRIOR APPLICATION DATA:
24     APPLICATION NUMBER:  US 08/081,070
25     FILING DATE:  22-JUN-1993
26     ATTORNEY/AGENT INFORMATION:
27     NAME:  Brady, John P.
28     REGISTRATION NUMBER:  39,118
29     REFERENCE/DOCKET NUMBER:  4600-0175,20/C19P101
30     TELECOMMUNICATION INFORMATION:
31     TELEPHONE:  (650) 324-0880
32     TELEFAX:  (650) 324-0860
33     INFORMATION FOR SEQ ID NO: 374:
34     SEQUENCE CHARACTERISTICS:
35     LENGTH: 50 base pairs
36     TYPE: nucleic acid
37     STRANDEDNESS: double
38     TOPOLOGY: linear
39     MOLECULE TYPE: DNA (genomic)
40     HYPOTHEICAL: NO
41     ORIGINAL SOURCE:
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Genotex version 4.5  
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OM nucleotide nucleotide search, using SW model

Run on: September 26, 2002, 09:00:36 : Search time 1767.99 Seconds

(without alignments)  
11420.565 Million Cp1 updates/sec

Letter: US-10-006-430-3  
1496  
Sequence: 1 ccaatgctgctggaagagcgc.....tgcctaaaaaanaaaaaa 1496

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Search: 13746237 seqs, 6748477542 residues

al number of hits satisfying chosen parameters: 88862

Minimum DB seq length: 16  
Maximum DB seq length: 50

Post processor: Minimum Match 08  
Maximum Match 100%

Listing first 45 summaries

EST: \*  
1: em\_est\_ba: \*  
2: em\_est\_hum: \*  
3: em\_est\_in: \*  
4: em\_est\_mus: \*  
5: em\_est\_ov: \*  
6: em\_est\_pl: \*  
7: em\_est\_ro: \*  
8: em\_est\_tc: \*  
9: qb\_est1: \*  
10: qb\_est2: \*  
11: qb\_est3: \*  
12: qb\_est4: \*  
13: em\_gss\_hum: \*  
14: em\_gss\_in: \*  
15: em\_gss\_pl: \*  
16: em\_gss\_vtl: \*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	42.4	2.2	49	10	B034637	B034637 B034637
2	27.6	1.8	50	12	A2456166	A2456166 IM0258B20
3	24.6	1.6	48	9	AL637106	AL637106 AL637106
4	24.4	1.6	50	12	A2787456	A2787456 2M0033006
5	24.2	1.6	46	12	A2777521	A2777521 2M0012B01
6	24.2	1.6	49	12	T433012P	T433012P
7	24.2	1.6	42	12	T664A10P	T664A10P
8	24.2	1.6	48	12	A2646447	A2646447
9	24.2	1.6	48	12	A2650456	A2650456 1M0520C09
10	24.2	1.6	48	12	A2860712	A2860712 2M0166D18
11	24.2	1.6	49	12	A2506149	A2506149 1M0347J05
12	24.2	1.6	49	12	A2656875	A2656875 1M0532M11
13	24.2	1.6	49	12	A2764533	A2764533 1M0560C17
14	24.2	1.6	49	12	A2773388	A2773388 1M0584E23
15	24.2	1.6	49	12	A2820100	A2820100 2M0092A12
16	24.2	1.6	49	12	T416R0390	T416R0390
17	24.2	1.6	50	9	AA120437	AA120437 mm47a11.f

C 18	24	1.6	50	10	B1491464	B1491464 d1041.000
C 19	24	1.6	50	12	A2358097	A2358097 1M0107008
C 20	24	1.6	50	12	A2816605	A2816605 2M0085K24
C 21	24	1.6	50	12	A2861629	A2861629 2M0166A19
C 22	24	1.6	50	12	A2967786	A2967786 2M0238F20
C 23	23.8	1.6	44	12	A342202	A342202 1M0075G11
C 24	23.8	1.6	44	12	A486433	A486433 1M0148N20
C 25	23.8	1.6	44	12	A2981881	A2981881 2M0262P23
C 26	23.6	1.6	46	9	AM332205	AM332205 S5E10 AGS
C 27	23.6	1.6	48	12	A2652813	A2652813 1M0545N08
C 28	23.4	1.6	49	12	A2335579	A2335579 1M0365A01
C 29	23.2	1.6	43	10	B1667675	B1667675 603293023
C 30	23	1.5	47	12	A2597378	A2597378 1M0411C24
C 31	23	1.5	47	12	A2769421	A2769421 1M0570001
C 32	23	1.5	47	12	A2851459	A2851459 2M0154P07
C 33	22.8	1.5	43	12	A2407933	A2407933 1M0176624
C 34	22.8	1.5	43	12	A2666812	A2666812 1M0447012
C 35	22.8	1.5	50	9	A0104216	A0104216 A0104216
C 36	22.6	1.5	50	9	AA574989	AA574989 vm44a0.1
C 37	22.6	1.5	49	12	A2826077	A2826077 2M0104A07
C 38	22.6	1.5	45	12	A2731900	A2731900 1M0360A03
C 39	22.6	1.5	45	12	A2442112	A2442112 1M0244R08
C 40	22.6	1.5	45	12	A2473613	A2473613 1M0289003
C 41	22.6	1.5	45	12	A2822082	A2822082 2M0095P05
C 42	22.6	1.5	45	12	A2325773	A2325773 1M0048112
C 43	22.6	1.5	46	12	A2407590	A2407590 1M0178A16
C 44	22.6	1.5	45	12	A2510203	A2510203 1M1454K06
C 45	22.6	1.5	46	12	A2650069	A2650069 1M1520105

## ALIGNMENTS

RESULT 1	B034637	49 bp	mRNA	linear	EST 06-1067-2001
LOCUS	B034637				
DEFINITION	B034637 NIH Mochii normalized Xenopus neurula library cDNA				
ACCESSION	B034637				
VERSION	B034637.1	GI:17392178			
KEYWORDS	EST				
SOURCE	Xenopus laevis				
ORGANISM	African clawed frog.				
REFERENCE	1 (bases 1 to 49)				
AUTHORS	Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, J. and Kohara, Y.				
TITLE	Expressed genes in X. laevis embryo				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Tadashi Shin-i Center for Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nig.ac.jp. Location/Qualifiers 1..49 /organism="Xenopus laevis" /db_xref="taxon:8355" /clone="X030621" /clone_11p="NIH Mochii normalized Xenopus neurula library" /issue_type="whole embryo" /dev_stage="stage 15" 10 a 12 c 10 g 16 t 1 others				
BASE COUNT	10 a 12 c 10 g 16 t 1 others				
ORIGIN					
Query Match	2.2%	Score 32.4	DB 10	Length 49	
Host local Similarity	83.7%	Prod. No. 2.1e-05			





## REFERENCE

1 (bases 1 to 49)

Hall, N., Bowman, S., Leonard, N.J., Joseph, J., Alkin, R., Chellinor, D., Ormond, D., Harris, R., El Sayed, N., Hou, L., McVittie, S., Kapur, M.A. and Barrett, J.B.C.

## JOURNAL

Submitted (10 Dec 2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrett@sanger.ac.uk and nll@sanger.ac.uk

## COMMENT

Constructed at the Institute for Genome Research (IGR), Hinxton, UK. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREP92/4 clonal 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v.3 method used for the library construction is described in detail in Smith, B. and Venter, J.C. (Makina small insert libraries for whole genome shotgun sequencing projects. In genome sequencing: A practical approach, eds. M. Vainin and B. Barrett, Oxford University Press, 1999).

Small, well-solved clones details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/TB/trypanosoma\\_brucei/](http://www.sanger.ac.uk/Projects/TB/trypanosoma_brucei/)

Location/Qualifiers

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## FEATURES

Location/Qualifiers

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DEFINITION	SEQUENCE	331	FROM	PATENT	US 5,726,014.
ACCESSION	U01134				
VERSION	U01134.1	GI: 5945603			
KEYWORDS					
SOURCE	UNKNOWN.				
ORGANISM	UNKNOWN.				
REFERENCE	UNKNOWN.				
ATTIBIOS	1 (bases 1 to 50)				
TITLE	Edwards, C. A., Cantor, C. R., Andrews, B. M. and Fry, L. M.				
DESCRIPTION	Screening assay for the detection of DNA-binding molecules				
FEATURES	Parent: US 5,726,014 A 191.10 MAR 1998;				
SOURCE	Location/Qualifiers				
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	/organism="unknown"				
BASE COUNT	4 a	14 c	42 g	1 t	
ORIGIN					
DEFINITION	SEQUENCE	331	FROM	PATENT <td>US 5,726,014.</td>	US 5,726,014.
ACCESSION	U01134				
VERSION	U01134.1	GI: 5945603			
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DEFINITION	SEQUENCE	331	FROM	PATENT <td>US 5,726,014.</td>	US 5,726,014.
ACCESSION	U01134				

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